16(745

Schreiber, David

From:

Sent:

Foley, Shanon Tuesday, August 02, 2005 8:04 AM Schreiber, David 10/808964

To:

Subject:

Hi David. Please search nt SEQ ID NO: 2 and its complement. Please also include an interference search.

Thank you. Shanon

(Uspło) Angle Blank (Uspło)

EST851004 EST841792 EST851203 EST853111 EST854689 EST854689 EST852278 EST852278

EST859131 EST783406 EST784510 EST840516

Scoring table:

Sequence:

Minimum DB Maximum DB

Database

OM nucleic

Run on:

EST859882

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Genoscope.

Direct Submission

Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 ENYE cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
- Determination of this BAC-ns.fr
- Determination of the Drosophila
- The BDGP is constructing a physicial map of the Drosophila
- Melanogaster genome using these BACs. For further information
- Dlease see http://www.fruitfly.org The BDGP Drosophila
- melanogaster BAC library was prepared by Kazuroyo Gosegawa and
- Aaron Mammoser in Pieter de Jong's laboratory in the Department of
- Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
- NY. The library is named RPCI-98 and was constructed by partial
- BCORI digestion of Drosophila DNA provided by the BDGP from the
- isogenic strain y2, cn bw sp, the same strain used for the BDGP's
- Pl and EST libraries. A more detailed description of the library
- and how to order individual BAC clones, the entire library, or
- filters for hybridization from the BACPAC Resource Center can be
- found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR48P19 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ALO78714
ALO78714.1 GI:5102004
GSS.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
CO413933
CV136509
CV144133
CV139795
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CV141902
CV141069
CV141069
CV14129
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    .1101
    /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
    /db_xref="taxon:7227"

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Pred. No. 0.00037;
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/note="end : TET3"
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VERSION
KEYWORDS
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AUTHORS
TITLE
JOURNAL
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GA Ea002
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BG445569 C
CD659610 I
AG365778 I
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CA741621 I
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CA222795

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Compugen Ltd
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                        GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                         nucleic search, using sw model
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BP162319
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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1773
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9b htc:..

9b est2:...

9b est4:...

9b est4:...

9b est6:...

9b 9s81:...
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GA Ba0028F15f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum carboreum carboreum cBNA clone GA Ba0028F15f, mRNA sequence.
                                                                                                                                                                                                                                                             1401 TACAATCCCCCAACCCTTCTCCTACCACTCCCGTTACTTCACACCCCAAACCTGTTGA 1460
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                                                                                                                                                                                               Gossýpium arboreum
bakaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Malvales, Malvaceae, Malvoideae, Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 870)
Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,
Wing,R.A., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
Unpublished (2000)
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/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                       438 MANAGADAYTTYANTTYANGADAYANGADAYAYADAYAYADAYANGADAYAYTYANAYAYAYATYANAYANAYANAYANAYAYANAYAYA
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/note="Vector: pBK-CMV; Site_l: BcoRI; Site_2: XhoI"
                                                                                                                                                                 1341 CTTTGTAACAAAGGCCACAGCCCTAACCTATGACCCATATGTAAACTACTCCCCGCCA
                                                                   Length 939;
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                                                                     2.8%; Score 50.2; DB 9; Length 9
Larity 16.5%; Pred. No. 0.023;
Conservative 120; Mismatches 98; Indels
                                                                DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4228
Pax: 864 656 4293
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/organma="Gossypium arboreum"
/mol_type="mRNA"
/strain="AKA"
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Seq primer: TAATACGACTCACTATAGGG
High quality sequence start: 6
High quality sequence stop: 659.
Location/Qualifiers
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/db_xref="taxon:29729"
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/note="end : TET3"
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                                                 1327 ATTCTAGATGATAACTTTGTAACAAAGGCCACAGCCCTAACCTATGACCCATATGTAAAC 1386
                                                                                                                                                1387 TACTCCTCCCGCCATACAATCCCCCAACCCTTCTCCTACCACTCCCGTTACTTCACACCC 1446
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1687 GTGATAACAAAAAGACTCAGTAATTTTATTTTATATGGGAAAA 1729
Conservative 138; Mismatches 178; Indels
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mol type="genomic DNA"
db xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (fruit fly)
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/clone="BACR26H16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genoscope
  87;
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DEFINITION
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TITLE
JOURNAL
    Matches
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CNS00CNG
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R.Site 1
R.Site 2
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                          Best Local Sim
Matches 104;
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     Query Match
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TITLE
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REFERENCE
AUTHORS
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/vorganism="Eimeria tenella"
/mol_type="mRNA"
/do_type="mRNA"
/do_type="mRNA"
/do_type="mRNA"
/do_type="mstan tenella"
/dov_stage="LS18"
/dev_stage="LS18"
/dab_host="E.coli DH10B (GeneHog, Invitrogen,Inc)"
/clone_lib="Eimeria tenella Ms-6 Excised cDNA"
/clone_lib="Simeria tenella Ms-6 Excised cDNA"
/note="Vector: pBluescript SK-; Site_l: BcoRI, Site_2:
Xhol; Sporozoites were obtained from in vitro sporulated
and excysted oocysts of E. tenella grown in chickens. cDNA
was synthesized from poly mRNA using an oligo-dT primer
containing a Xhol site. Following second strand synthesis,
EcoRI adapters were ligated to the cDNA and products were
size-selected on sephacryl SSOO. The cDNA and products were
size-selected on sephacryl SSOO. The cDNA were ligated to
EcoRI/Xhol prepared lambda ZapII (Stratagene). The primary
library was mass excised using ExAssist helper phage
(Stratagene). The phagemids were precipitated with PEG
8000, extracted with phenol/chloroform and electroporated
into DH10B cells. The library may contain a small
percentage of host or bacterial contaminants. Library
materials provided by: Paul Liberator, Merck Research Labs
Libbary constructed by: Paul Liberator, Merck Research
Labs."
                                                                             1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD659610 573 bp mRNA linear BST 19-JUN-2003
BEESTPE53d09.y1 Eimeria tenella M5-6 Excised cDNA Eimeria tenella
CDNA 5', mRNA sequence.
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                                                                                                                                                                             1054 CGCCACCGCTACCGTTGGAGGAAAATGGCATCTTCAACACCCGCCTCTCCCGCACC 1113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
Contact David Sibley (toxoest@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Seg primer: -40RP from Gibco.
                                                                                                                             508
                                                                                                                                                                                                                             507 CCCCCCCCCCCCCANNINNNNNNNNNNNNGNNNNCNCCACCACCATACCCTCCACCATT 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liberator, P., Diaz, C., Tang, K., Marra, M., Hillier, L., Kucaba, T., Martin, J., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, B., Köhn, S., Florence, N., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., Wilson, R. and
                                                                             994 CACCGCCCCCCGCAGCCATCTTGGCCAGATCCTCCGCCGCCGCCCCTGGCTCGTCCACCCC
                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WashU-Merck Eimeria tenella project
Unpublished (1999)
Contact: David Sibley, Ph.D.
WashU-Merck Eimeria tenella project
WashU-Merck Eimeria tenella project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fex: 314 286 1800
                          ö
                                                                                                                                                                                                                                                                                  1114 TTCGGATATACTGTCAAGGCTACCACAGTCAGAACGCCCTCCTGGGC 1160
                                                                                                                                                                                                                                                                                                                                   447 recerarceaecrreaesecereeeceaecarareereereses
48.5%; Pred. No. 0.063;
tive 0; Mismatches 86; Indels
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                          81; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eimeria tenella
Best Local Similarity
Matches 81; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eimeria.
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JOURNAL
COMMENT
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ORIGIN

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Direct Louison.

S Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.

B Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.

Direct Submission

Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Taurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gac.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-911, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
                                                           ö
                                                                                                                                                                                                                                                                                                                                                  AG365778 1141 bp DNA linear GSS 03-JUN-2004 mus musculus molossinus DNA, clone:MSMg01-168K18.TJ, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                    294 gadanggagcagcagcanccicancangcinincagcginacciningcagcagcagas
                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                            354 GCAGCAGCAGCCACACACCCGCCGCTGCCGCCCCTGTCCCCAACAGCAGCAGCAGTCGCG
                                                                                                                                                                                                                                   980 ACCGCAGAAGAAGACACCGCCCCCGCAGCCATCTTGGCCAGATCCTCCGCCGCCGCCCTT
                                                                                                                    920 GTAATACTACAGCAGCGCACTTCTTTCACTTTTATAGGATGACGTATCCAAGGAGGCGTT
                                                           Gaps
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2.7%; Score 48.2; DB 6; Length 573;
larity 52.8%; Pred. No. 0.074;
Conservative 0; Mismatches 93; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue type="mixture of kidney and spleen"
/clone lib="MSMg01 Mouse Male BAC Library"
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35.2%; Pred. No. 0.13;
tive 0; Mismatches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          474 AGCTTCCCCCCTCTGC 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus molossinus
Mus musculus molossinus
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: EcoRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 95; Conservative
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LIBRARY
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S71 bp mRNA linear EST 26-NOV-2002 wialc.pk003.e22 s' end, mRNA sequence.
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                                               1415 CCTTCTCCTACCACTCCCGTTACTTCACACACAAACCTGTTCTTGACTCCACCATTGATT 1474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
XhoI; Wheat (Triticum aestivum, Hi Line) immature anthers"
                                                                                                                                           1475 ACTICCAACCAAATAACAAAAGGAATCAGCITIGGATGAGGCTACAAACCTCTAGAAATG 1534
                                                                                                                                                                 1535 TGGACCACGTAGGCCTCGGCACTGCGTTCGAAAACAGTATATACGACCAGGACTACAATA 1594
                                                                                                                                                                                                                                                                1595 TCCGTGTAACCATGTATGTACAATTCAGAGAATTTAATCTTAAAGACCCCCCACTTAAAC 1654
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659 MCCCAACAMMCMCACACAMAAMAMAMAAMMAAMMAACMCAAMMACMC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Triticum aestivum (bread wheat)
Triticum aestivum
Triticum aestivum
Bukaryota; Viridiplantaea; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z., Miao, G., Caraher, N. and Hanafey, M.K.
Unbort Wheat cDN Sequence
Unpublished (2002)
Contact: Scott V. Tingey
                                                                                                                                                                                                                                                                                                                                                                                                                                  1515 CCTAAATGAATAAAATAAAAACCATTACGATGTGATAACAAAAAAGACTCAGTAA 1710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      325 CCTCCTCCAGATCCGCCTCCGCCTCCTCCAGAACCGCCTCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGCAGAAGAAGACACCGCCCCCCGCAGCCATCTTGGCCAGATCCTCCGCCGCCGCCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           E. I. DuPont de Nemours and Company
I. Imnovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2602
Email: Scott.V.Tingey@USA.dupont.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6; Length 571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Triticum aestivum"
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58.1%; Pred. No. 0.21;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:4565"
/clone="wialc.pk003.e22"
/tissue_type="anthers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="wialc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab host="DH10B
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- Web : www.genoscope.cns.fr)
- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Googgawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp. the same strain used for the BDGP's pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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ALO66784
ALO66784.1 GI:4945247
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                                                         Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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|mol_type="genomic DNA"
|db_xref="taxon:7227"
|clone="BACR44009"
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/note="end : TET3"
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- Web: www.genoscope.cns.fr)
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Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila denome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecoll digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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BP 191 91006 BVRY cedex - FRANCE (B-mail : segref@genoscope.cns.fr
                                                                                                                  Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/mol_type="genomic DNA"
/db_xref="texon:7227"
/clone="BACR39G08"
/clone=lib="RPCI-98"
/note="end : TET3"
fly), genomic survey sequence.
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(CB 1 (bases 1 to 857)
(CB Uenish!, H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H., Okumura,M., Hamasima,N. and Awata,T.

PEDE (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries

Nucleic Acids Res. 32 (1), D484-D488 (2004)

Contact: Hirohide Uenishi
Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan

Tel: +81-29-818-8627

Email: huenishi@affrc.go.jp

EST project with full-length enriched cDNA libraries carried out in Animal Genome Research Program (Japan) by National Institute of Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
                                                                                                                                                                                                             BP162319 full-length enriched swine cDNA linear EST 30-DEC-2003 BP162319 full-length enriched swine cDNA library, adult thymus Sus scrofa cDNA clone THY010093C05 5', mRNA sequence.
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|dev_stage="adult"
|clone_lib="full-length enriched swine cDNA library, adult
thymus"
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quality bases were trimmed based on the quality values.
Location/Qualifiers
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/db_xref="taxon:9823"
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Length 909;
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  2.6%; Score 46.6; DB 9;
ilarity 22.6%; Pred. No. 0.23;
Conservative 118; Mismatches 190;
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CNSOOJTL 909 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR39G08 of RPCI-98 library from Drosophila melanogaster (fruit

LOCUS

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AW255252.1 GI:7244504
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//clone_lib="PL4"
//olone="Organ: Developed inflorescence and rachis
//note="Organ: Developed inflorescence and rachis
(20cm-long); Vector: pSport1; Site_1: Sal1; Site_2: NotI;
An unidirectional cDNA library generated from [Developed inflorescence and rachis (20cm-long)]. cDNA was prepared from poly4+ mRNA using SuperScript Plasmid System Kit
(Invircem): The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
                                                                         CA222795 560 bp mRNA linear EST 25-SEP-2003
SCEZFL4038H05,g FL4 Saccharum officinarum cDNA clone SCEZFL4038H05
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Clone distribution: clone distribution information can be found
through the Brazilian clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 038 row: H coluun: 05
Seq primer: T7 Promoter Primer.
Location/Qualifiers
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Vettore, A.L., da Silva, F.R., Kemper, B.L. and Arruda, P. The libraries that made SUCEST
Genet. No. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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Universidade Estadual de Campinas
Gaixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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/clone="SCEZFL4038H05"
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                                                                                                                                              5', mRNA sequence.
CA222795
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AW25252 401 bp mRNA linear EST 23-AUG-2000 ML252 peppermint glandular trichome Mentha x piperita cDNA, mRNA sequence.

DEFINITION

AW255252

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Enkaryota; Viridiplantae; Streptophyta; Enkaryota; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. B. 1 (bases 1 to 460)

Sequencing of ESTs from loblolly pine embryonic libraries
Unpublished (2004)

Contact: C. Robin Buell
Plant Genomics Group
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: rbuell@tigr.org
This clone is available through TIGR. Please contact pine@tigr.org
for further information
                                                                                                                                                                                                                                                                                               Probing essential oil biosynthesis and secretion by functional evaluation of expressed sequence tags from mint glandular trichomes Proc. Natl. Acad. Sci. U.S.A. 97 (6), 2934-2939 (2000)
                                                                                                                                                                                                                                   1 (bases 1 to 401)
Lange, B.M., Wildung, M.R., Stauber, E.J., Sanchez, C., Pouchnik, D. and
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EST.

Mentha x piperita (peppermint)

Mentha x piperita

Mentha x piperita

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamiids; Lamiales; Lamiaceae; Nepetoideae; Nepeteae;
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EST855400 Sequencing ESTs from loblolly pine embryos Pinus taeda cDNA clone RPID242 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Lange, B.M.
Institute of Biological Chemistry/Washington State University
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Best Local Similarity 55.7%; Pred. No. 0.28;
Matches 88; Conservative 0; Mismatches 70; Indels
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/cultivar="Black Mitcham"
/db_xref="taxon:34256"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pullman, WA
Email: lange-m@mail.wsu.edu.
Location/Qualifiers
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Pinus taeda
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Query Match
Best Local Similarity 68.9
Matches 62; Conservative
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                                                                                                                                                                                                  /db_host="Ecoli DH10B-TonA"
//lone="RFDD242"
//lab_host="E.coli DH10B-TonA"
//clone|lb="Sequencing RSTB from lobblolly pine embryos"
//clone|lb="Sequencing RSTB from lobblolly pine embryos"
//clone|Sequencing RSTB from lobblolly pine embryos"
//note="Organ: Zygotic Embryo and Megagametophyte; Site_1:
ECORY, tissue: Mhole megagametophytes isolated from pine
seeds Whole embryos excised from these megagametophytes,
whole somatic embryos excised from these megagametophytes,
whole somatic embryos excised from these megagametophytes,
sused for library construction. Pine cones were harvested
weekly from open-pollinated 7-56 mother trees, collections
occurred from 7/01/02 until 10/15/02. Whole
megagametophytes were first isolated from pine seeds, and
whole embryos excised from these megagametophytes each was
flash frozen. Embryo development was assessed using the
system of Pullman et al [Pullman GS, Johnson S, Peter G,
Cairney J, Xu N. 2003. Loblolly Pine somatic
embryogenesis development of a maturation medium and
resulting embryo quality. Plant Cell Reports 21:747-758
(http://link.springer.de/link/service/journals/00299/conte
nts/03100586/). For photographs see Clavatta et al 2001.
(Ciavatta VT, Morillon R, Pullman GS, Chrispeels M,
Cairney J. 2001. An aquaglyceroporin is abundantly
expressed early in the development of the suspensor and
the embryo proper of loblolly pine (Pinus taeda L.). Plant
Physiol. 127: 1556-1567
(http://www.plantphysiol.org/cgi/content/full/127/4/1556))
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Buell, C.N., Hsiao, J. and Cairney, J.
Sequencing of ESTS from loblolly pine embryonic libraries
Unpublished (2004)
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The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
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Seg primer: ATT TAG GTG ACA CTA TAG.
                                                                                'organism="Pinus taeda"
                      Socation/Qualifiers
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Matches 62; Conserv
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AUTHORS
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COMMENT
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/lab.host="Scoil DH10B-TonA"
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ECORV; tisue: Whole megagametophytes jendled from pine
seeds, Whole embryos excised from these megagametophytes,
whole somatic embryos and suspensor tisuue from pine
culture, isolated from cell line Al2. Pooled RNA from
zygotic embryos and suspensor tisuue from tissue
culture, isolated from cell line Al2. Pooled RNA from
zygotic embryos and suspensor tissue from tissue
seed for library construction. Pine cones were harvested
weekly from open-pollinated 7-56 mother trees, collections
occurred from 7/01/20 until 10/15/02. Whole
megagametophytes were first isolated from pine seeds, and
whole embryos excised from these megagametophytes and
whole embryos excised from these megagametophytes and
flash frozen. Embryo development was assessed using the
system of Pullman et al (Pullman GS, Johnson S, Peter G,
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embryogenesis: development of a maturation medium and
resulting embryo quality, Plant Cell Reports 21:747-758
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nts/03/00586/). For photographs see Ciavatta et al 2001.
(Ciavatta VT, Morillon R, Pullman GS, Chrispeels M,
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expressed early in the development of the suspensor and
the embryo proper of loblolly pine (Pinus taeda L.). Plant
Physiol. 127: 1556-1567
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Buell, C. R., Hsiao, J. and Cairney, J. Sequencing of ESTs from loblolly pine embryonic libraries Unpublished (2004)
Contact: C. Robin Buell
Plant Genomics Group
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
This clone is available through TICR. Please contact pine@tigr.org for further information.
Location/Qualifiers
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                                                                                                                                                               organism="Pinus taeda"
                                                                                                                                                                                                                                                                                  Lyons, Georgia, USA"
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Embryo; Vector: pCWV-SPORT 6.1; Site 1: Not!; Site 2:
EcoRV; tissue: Whole megagametophytes isolated from pine
seeds, Whole embryos excised from these megagametophytes,
whole somatic embryos and suspensor tissue from tissue
culture, isolated from cell line Al2. Pooled RNA from
zygotic embryos, megagametophytes, and somatic embryos was
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embryogenesis: development of a maturation medium and
resulting embryo davelopment of a maturation medium and
resulting embryo davelopment of staturals/00299/conte
nts/03/0586/). For photographs see Ciavatta et al 2001.
(Ciavatta VT, Morillon R, Pullman GS, Chrispeels M,
Cairney J. 2001. An aquaglyceroporin is abundantly
expressed early in the development of the suspensor and
the embryo proper of loblolly pine (Pinus taeda L.). Plant
Physiol. 127: 1556-1567
(http://www.plantphysiol.org/cgi/content/full/127/4/1556))
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Email: rbuell@tigr.org
This clone is available through TIGR. Please contact pine@tigr.org
for further information
Seg primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
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Buell, C.R., Hsiao, J. and Cairney, J. Sequencing of ESTs from loblolly pine embryonic libraries
                                                                                                                                                                                                                            /mol_type="mRNA"
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Lyons, Georgia, USA"
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68.9%; Pred. No. 0.53;
iive 0; Mismatches 28; Indels
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                                                                                                                                                                                                  organism="Pinus taeda"
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Pinus taeda
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Contact: C. Robin Buell
Plant Genomics Group
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Best Local Similarity 68.9
Matches 62; Conservative
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/dobost="Relation"
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The Institute for Genomic Research 9712 Medical Center Dr. Rockville, MD 20850, USA Email: rbuell@tigr.org
This clone is available through TIGR. Please contact pine@tigr.org for further information Seq primer: ATT TAG GTG ACA CTA TAG.
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                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/culfivar="7-56 mother tree, open-pollinated tree from,
Lyons, Georgia, USA"
/db_xref="taxon:3352"
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                                                                                                                                                                                                                          Location/Qualifiers
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nes 62; Conserv
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Search completed: August 5, 2005, 06:31:56 Job time : 5981 sec8

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
               Copyright
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nucleic search, using sw model OM nucleic

Run on:

August 4, 2005, 21:48:07; Search time 981 Seconds (without alignments) 10698.982 Million cell updates/sec

US-10-808-964A-2 1773

Title: Perfect score:

1 ggtacctccgtggattgttc.....caaatcggccttcgggtacc 1773 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 seqs, 2959870667 residues

Searched:

8780412 Total number of hits satisfying chosen parameters:

seg length: 0 seg length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

N. Geneseq 16Dec04;*
1: geneseqn1980s;*
2: geneseqn1990s;*
4: geneseqn2000s;*
5: geneseqn2001as;*
6: geneseqn2001bs;*
6: geneseqn2001bs;*
8: geneseqn2003as;*
9: geneseqn2003as;* geneseqn2003cs:*geneseqn2003ds:*geneseqn2004as:*geneseqn2004bs:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

* Regult

Description .	Aal57177 Porcine c	Abx08205 PMWS-Porc	Abx08203 PMWS-Porc	Abx08207 CT-Porcin	Abx08206 CT-Porcin	Abx08204 PMWS-Porc	Abx08219 PMWS-Porc	Abx08202 PMWS-Porc	Abx08208 CT-Porcin	Abx08220 PK-15-Por	Aah74867 Nucleotid	Abx94361 Rolling c	Aah74865 Nucleotid	Abx94355 Rolling c	Aah74866 Nucleotid	Abx94356 Rolling c	Aaf75839 DNA fragm	Aal57176 Porcine c	Aax35013 Nucvleoti	Aaf28320 pJP107 do	
ΙD	AAL57177	ABX08205	ABX08203	ABX08207	ABX08206	ABX08204	ABX08219	ABX08202	ABX08208	ABX08220	AAH74867	ABX94361	AAH74865	ABX94355	AAH74866	ABX94356	AAF75839	AAL57176	AAX35013	AAF28320	
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Match	100.0	72.5	72.1	72.0	71.9	71.9	71.7	70.6	68.7	68.3	67.5	67.5	67.4	67.4	67.4	67.4	59.8	59.7	59.5	59.4	
Score	1773	1285.2	1278.8	1277.2	1274	1274	1270.8	1252	1218.2	1210.2	1196.8	1196.8	1195.8	1195.8	1195.8	1195.8	1059.8	1058.4	1055.6	1053.2	
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4 4 4 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	
	4 4 4 5 5 4 5

ALIGNMENTS

RESULT 1

Porcine circovirus type 2, PCV1-2; PCV1; PMWS; weaning piglet; dyspnoea; progressive weight loss; postweaning multisystemic wasting syndrome; ds; tachypnea; anaemia; diarrhoea; jaundice; virucide; vaccine; PCV2; gene; viral infection; chimeric. Porcine circovirus type 1-2 chimeric DNA. AAL57177 standard; DNA; 1773 BP. (revised)
(first entry) 27-0CT-2003 09-0CT-2003 AAL57177; AAL57177

Porcine circovirus type 1. Porcine circovirus type 2. Chimeric.

Location/Qualifiers 958. .1659 /*tag= a /product= "Porcine circovirus type 2 ORP2 capsid protein"

WO2003049703-A2

19-JUN-2003

11-DEC-2002; 2002WO-US039646.

12-DEC-2001; 2001US-0340775P. 08-NOV-2002; 2002US-0424340P. 09-DEC-2002; 2002US-00314512.

(VIRG) VIRGINIA TECH INTELLECTUAL PROPERTIES. (IOWA) UNIV IOWA STATE RES FOUND INC.

Meng X, Fenaux M, Halbur PG;

WPI; 2003-513959/48. P-PSDB; AAO23063.

New infectious chimeric nucleic acid molecule of porcine circovirus, useful for preventing and/or treating pigs against viral infection and/or postweaning multisystemic wasting syndrome.

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9; 85pp; English Claim 13; Fig The invention relates to a novel infectious chimeric nucleic acid molecule of porcine circovirus (PCV1-2) which comprises a nucleic acid encoding an infectious, non-pathogenic PCV1 (porcine circovirus type 1) containing an immunogenic open reading frame (ORF) gene of a pathogenic containing an immunogenic open reading frame (ORF) gene of a pathogenic provide circovirus type 2) in place of a PCV1 ORF gene. Postweaning multisystemic wasting syndrome (PWMS) is a complex disease of weaning piglets that is becoming increasingly more widespread. The condition poses a potentially serious economic threat to the swine industry, thus causative agent of PWMS. PWMS mainly affects pigs between 5-18 weeks of causative agent of PWMS. PWMS mainly affects pigs between 5-18 weeks of age and clinical symptoms include progressive weight loss, dyspnoea, tachypnea, anaemia, diarrhoea and jaundice. The chimeric polynucleotide of the invention demonstrates virucide activity and may be utilised as a vaccine for PWMS. The methods and compositions of the present invention may be useful for the prevention and/or treatment of pigs against viral lifection and/or PWMS. The current sequence is that of the PCV1-2.

Sequence 1773 BP; 472 A; 511 C; 359 G; 431 T; 0 U; 0 Other;

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240 540 120 CTGGTAATCAAAATACTGCGGGCCAAAAAAGGAACAGTACCCCCTTTAGTCTCTACAGTC 180 240 360 360 420 420 480 480 600 TAGAGAGCTTCTACAGCTGGGACAGCTGAGGAGTACCATTCCTGGGGGCCTGATTG 120 9 Acadroaccados de Acados de GGGCCCACTATGACGTGTACAGCTGTTCCCAATCACGCTGCTGCATCTTCCCGGCTCACT GGGCCCACTATGACGTGTACAGCTGTTCCAATCACGCTGCTGCATCTTCCCGCTCACT TAGAGAGCTTCTACAGCTGGGACAGCAGTTGAGGAGTACCATTCCTGGGGGGCCTGATTG CTGGTAATCAAAATACTGCGGGCCAAAAAAGGAACAGTACCCCCTTTAGTCTCTACAGTC AATGGATACCGGTCACACAGTCTCAGTAGATCATCCCAAGGTAACCAGCCATAAAAATCA TCCAAAACAACTTCTTCTCCATGATATCCCATCCCACCTTATTTCTACTAGGCTTC TACGGCCCACTGCCTCTTCCCACAACCGGGC TACGGGCCCACTGGCTCTTCCCCACAACCGGGC TTCAAAAGTTCAGCCAGCCGCGGAAATTTCTCACATACGTTACAGGAAACTGCTCGGCT ACAGTCACCAAAGACCCCGTCTCCAAAAGGGTACTCACAGGTAGTAGACAGGTCGCTGCGC GTATGTGGCCTTCTTTACTGCAGTAT GGTACCTCCGTGGATTGTTCTCCAGCAGTCTTCCAAAATTGCAAAGTAGTAATCCTCCGA Gaps ö 9; Length 1773; 0; Indels B Query Match 100.0%; Score 1773; Best Local Similarity 100.0%; Pred. No. 0; Matches 1773; Conservative 0; Mismatches CAGTAGGTGTCCCTAGGCTCAGCAAA CAGTAGGTGTCCCTAGGCTCAGCAAAA 61 181 481 541 61 121 121 181 241 241 301 301 361 361 421 421 481 541 601

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The invention describes an isolated nucleic acid (I) from a porcine circovirus (PCV) where (I) comprises a sequence coding for a circovirus colypeptide. A vaccine comprising a PCV nucleic acid that encodes an immunogenic polypeptide of type I or type II PCV strain and a carrier, is useful for treating or preventing congenital tremors in a pig or its progeny (PCV type I is composed of PR-15-PCV and CT-PCV-P7; PCV type II is composed of PRWS-PCV-P2, -P3, -P4, and CT-PCV-P5, -P6).

An isolated PCV strain (II) is useful for diagnosing a pathological cause of congenital tremors in a pig which involves determining whether the pig congenital tremors in a pig which involves determination of a congenital tremors in a pig which involves determination of a congenital sample from the pig, by detecting hybridisation of an oliopical sample from the pig, by detecting hybridisation of an oliopical sample from the pig by detecting the presence of PCV polypeptide in a biological sample from the pig. An expression vector (III) encoding a colypeptide is useful as a vector vaccine against congenital tremors.

(II) along with a suitable adjuvant is useful as a whole PCV vaccine, while the antigenic PCV polypeptides are useful in passive in a proportion of the pig and the prosence of antibodies as useful as a whole PCV vaccine, while the antigenic PCV Polypeptides are useful as a whole PCV vaccine, imministic congenital pression of imministrations of incoming a propried in the prosence of antibodies are useful as a whole PCV vaccine, imministration against congenital province imministration and province in a province in a province or an expension are the province or in the province or in the pig publication and the province or in the province or in the province or in the pig publication and province or in the pig publication and province or in the province or in the pig publication and province or in the pig publication and province or in the pig publication and publication and province or in the pig publication and publication and p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New porcine circovirus (PCV) nucleic acids for use as a component of vaccines for treating or preventing congenital tremors in pigs.
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                                                                                                                                                                                                                                                                                                                                                        Porcine circovirus genome; PCV; vaccine; type I PCV strain; type II PCV strain; congenital tremor; pig; whole PCV vaccine; passive immunisation; ds.
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Pred. No. 0;
0; Mismatches 158; Indels
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                           1741 GGGTCCACTGCTTCAAATCGGCCTTCGGGTACC 1773
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GGGTCCACTGCTTCAAATCGGCCTTCGGGTACC
                                                                                                                                                                                                                                                                                                                  PMWS-Porcine circovirus (PCV) P4 genome.
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                                                                                                                                                                                                                          New porcine circovirus (PCV) nucleic acids for use as a component of vaccines for treating or preventing congenital tremors in pigs.
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N-PSDB; ABU02903, ABU02914, ABU02918, ABU02925, ABU02934, ABU02937,
ABU02944, ABU02951, ABU02962, ABU02967.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     circovirus genome; PCV; vaccine; type I PCV strain; PCV strain; congenital tremor; pig; whole PCV vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kanitz CL;
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The invention describes an isolated nucleic acid (I) from a porcine circovirus (PCV) where (I) comprises a sequence coding for a circovirus (CC circovirus (PCV) where (I) comprising a PCV nucleic acid that encodes an immunogenic polypeptide of type I PCV strain and a carrier, is useful for treating or preventing congenital tremors in a pig or its progeny (PCV type I is composed of PK-15-PCV and CT-PCV-P7; PCV type II composed of PMWS-PCV-P1, PWWS-PCV-P2, -P3, -P4, and CT-PCV-P5, -P6).

An isolated PCW strain (II) is useful for diagnosing a pathological cause of congenital tremors in a pig which involves determining whether the pig consening expensive the pig by detecting the presence of a PCV nucleic acid in a biological sample from the pig, by detecting hybridisation of an oligonucleotide. Optionally, the determination of infection is effected by detecting the presence of polypeptide in a biological sample from the pig by detecting the presence of antibody that specifically binds a PCV polypeptide in a biological sample of the pig. An expression vector (III) encoding a PCV polypeptide is useful as a vector vaccine against congenital tremore. (II) along with a suitable adjuvant is useful as a whole PCV vaccine, while the antigenic PCV polypeptides are useful in passive communication strategies. This sequence represents a porcine circovirus
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Pred. No. 0;
0; Mismatches 162; 1
                  Claim 1; Page 83; 88pp; English
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Best Local Similarity 88.8%;
Matches 1458; Conservative
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The invention describes an isolated nucleic acid (I) from a porcine circovirus (PCV) where (I) comprises a sequence coding for a circovirus polypeptide. A vaccine comprising a PCV nucleic acid that encodes an immunogenic polypeptide of type I or type II PCV strain and a carrier, is useful for treating or preventing congenital tremors in a pig or its progeny (PCV type I is composed of PWAS-PCV-PJ, PWAS-PCW-PJ, PWAS-PCW-PWAS-PCW-PJ, PWAS-PCW-PJ, PWAS-PCW-PJ, PWAS-PCW-PJ, PWAS-PCW-PJ, PWAS-PCW-PWAS-PCW-PWAS-PCW-PWAS-PCW-PWAS-PCW-PWAS-PCW-PWAS-PWAS-
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ABU02948, ABU02955, ABU02960, ABU02966, ABU02968.
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                                                                                                                                                                                                                                                      circovirus genome; PCV; vaccine; type I PCV strain; PCV strain; congenital tremor; pig; whole PCV vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kanitz CL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Choi J, Kiupel M,
                                                                                                                                                                                                       CT-Porcine circovirus (PCV) P6 genome.
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72.08;
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Best Local Similarity 88.7
Matches 1457; Conservative
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	ABXO8206/C ID ABXO8206 standard; DNA; 1768 BP. AC ABXO8206 standard; DNA; 1768 BP. AC ABXO8206; XX ABXO8206; XX CT-Porcine circovirus (PCV) P5 genome. XX CT-Porcine circovirus genome; PCV; vaccine; type I PCV strain; congenital tremor; pig; whole PCV vaccine; XX WOZ00196377-A2. XX PORCINE circovirus. XX WOZ00196377-A2. PD 20-DEC-2001. XX X X
195 ACACAGTCTCAGTACATCCAAGGTAACCAGCCATAAAATCATCCAAAACACACAC	

The invention describes an isolated nucleic acid (I) from a porcine circovirus (PCV) where (I) comprises a sequence coding for a circovirus (CC Diypelide. A vaccine comprising a PCV nucleic acid that encodes an immunogenic polypeptide of type I or type II PCV strain and a carrier, is progeny (PCV type I is composed of PK-15-PCV and CT-PCV-P7). PCV type II is composed of PMS-PCV-P2, -P3, -P4, and CT-PCV-P5. PF0.

An isolated PCV strain (II) is useful for diagnosing a pathological cause of congenital tremors in a pig which involves determining whether the pig has been infected by PCV strain type I or type II. The determination of the infection is effected by detecting the presence of a PCV nucleic acid in a biological sample from the pig, by detecting hybridisation of an oligonucleotide. Optionally, the determination of infection is effected by detecting the presence of PCV polypeptide in a biological sample from the pig by detecting the presence of an antibody that specifically binds a PCV colympatide. Optionally, the determination of infection is effected by detecting the presence of an antibody that specifically binds a PCV colympatide is useful as a vector vaccine against a PCV polypeptide in a biological sample of the pig. An expression vector (III) encoding a CC (II) along with a sultable adjuvant is useful as a whole PCV vaccine, while the antigenic PCV polypeptides are used as components of subunit vaccines. Antibodies against PCV proteins are useful in passive immunisation strategies. This sequence represents a porcine circovirus

Sequence 1768 BP; 451 A; 361 C; 497 G; 459 T; 0 U; 0 Other;

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1649 1589 1529 1469 1349 1229 1169 CAGCCGCGGAAATTTCTGACAACGTTACAGGGTGCTGCTCTGCAACGGTCACCAGACT 1409 494 434 554 674 135 ACTGCGGGCCAAAAAGGAACAGTACCCCCTTTAGTCTCTACAGTCAATGGATACCGGTC ACACAGTCTCAGTAGATCATCCCAAGGTAACCAGCCATAAAAATCATCCAAAACAACAAC TTCTTCTCCATGATATCCATCCCACTTATTTCTACTAGGCTTCCAGTAGGTGTCCCT Trefrenceargerancearceaecaecaecarretreragergerreeagrangergerree AGOCTICAGONANATTACGGGCCCACTGGCTCTTCCCCACAACCGGGCGGGCCCACTATGAC ceegrerecaaaarrageaececarragerriraceaececeaeereece GTGTACAGCTGTTCCAATCACGCTGCTGCATCTTCCCCGCTCACTTTCAAAAGTTCAGC Grenacarnegrerrecaarcacecrrerecarrireceeercacrricaaaagrreage CAGCCCCCCGGAAATTTCTCACATACGTTACAGGAAACTGCTCGGCTACAGTCACCAAAGA CCCCGTCTCCAAAAGGGTACTCACAGCAGTAGACAGGTCGCTGCCTTCCCCTGGTTCCG 1348 AGGAGCTCCACATTCAATAAGTAAGTTGCCTTCTTTACTGCAATATTCTTTATTCTGCTG GTCGGTTCCTTTCGCTTTCTCGATGTGCGGCGCGCCCAAAATACCACTTCACCTTGTT 1288 ATCAGTTCCTTTGGCTTTCTCGATGTGGCGGGGGGCACCCAAATACCACTTCACTTATT AAAAGTCTGCTTCTTAGCAAAATTCGCAAACCCCTGGAGGTGAGGAGTTCTACCCTCTTC Gaps 22; Score 1274; DB 6; Length 1768; Pred. No. 0; 0; Mismatches 165; Indels 71.9%; Matches 1455; Conservative Similarity 195 1708 1648 315 1588 1528 (1408 675 1768 1468 615 255 375 435 555 495 Query Match Local 8 8 8

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RESULT 6 ABX08204/c

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735 CAAACCTTCCTCGCCACAAACAAAATCAAAAAGGAGATTGGAAGCTCCCGTATTTT

1141 1201 1321 1381 1741 1168 ATTACCCTCCTCGCCAACAATAAATAATCAAATAGGGAGATTGGGAGCTCCCGTATTTT 1109 1021 1081 1261 1441 1501 1561 1621 1681 812 692 632 572 961 932 452 392 272 215 CTGTTATTCTAGATGATAACTTTGTAACAAAGGCCACAGCCCTAACCTATGACCCATATG GCCGCTT-----TTCTTGCTTGGCATTTT----CACTGACGCTGCCGAGGTGCTGC CGCTGCCGAAGTGCGCTGGTAATACTACAGCAGCGCACTTCTTTCACTTTTATAGGATGA CGTATCCAAGGAGGCGTTACCGCAGAAGACACGCCCCCCGCAGCCATCTTGGCCAGA 811 ATGGCATCTTCAACACCGCCTCTCCGCACCTTCGGATATACTGTCAAGCGTACCACAG CGGGAGGGGGCCCAACAAAATCTCTATACCCTTTGAATACTACAGAATAAGAAAAGTTA AGGITGAATITCIGGCCCTGCTCCCCCATCACCCAGGGTGATAGGGGAGTGGCTCCACTG CTGTTATTCTAGATGATAACTTTGTACCAAAGGCCAATGCCCTAACCTATGACCCATATG 1382 TAMACTACTCCCGCCATACAATCCCCCAACCCTTCTCCTACCACTCCCGTTACTTCA TCCTCCGCCGCCCCCTGGCTCGTCCACCCCCCGCCACCGCTACCGTTGGAGAAAAA ATGGCATCTTCAACACCCGCCTCTCCCGCACCTTCGGATATACTGTCAAGGCTACCACAG TCAGAACGCCCTCCTGGGCGGTGGACATGATGAGATTTAATATTGACGACTTTGTTCCCC TCACAACGCCCTCCTGGGCGGTGGACATGAGATTTAAGCTTGACGACTTTGTTCCCC CGGGAGGGGGCCAACAAATCTCTATACCCTTTGAATACTACAGAATAAGAAAGGTTA TABACTACTICCIGCCATACAATCCCCCAACCTTTCTCCTACCACTCCCGTTACTTCA AGCTTTGGATGAGGCTACAAACCTCTAGAAATGTGGACCACGTAGGCCTCGGGACTGCGT GAGAATTTAATCTTAAAGACCCCCCACTTAACCCCTAAATG---AAAAATAAAAACCATT ACGATGTGATAACAAAAAGACTCAGTAATTTATTTTATATGGGAAAAGGGCACAGGGTG AGCTTTGGCTGAGGCTACAAACCTCTAGAAATGTGGACCACGTAGGCCTCGGCACTGCGT GAGAATTTAATCTTAAAGACCCCCCACTTAAACCCTAAATGAATAAAAATAAAAACCATT GGGAAAGGGTGACGAACTGGCC 136 1742 GGTCCACTGCTTCAAATCGGCC 855 1082 751 1262 391 988 1022 1442 1502 902 962 1142 1202 1322 1562 331 1622 271 931 691 571 511 451 a 셤 셤 ò 셤 g 셤 요 셤 ò 8 ò ò Š ద ठ 8 g 셤 ઠે g g 요 a ð 8 ò ઠે 8 ઠે 8 8 Š

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An isolated PCV strain (II) is useful for diagnosing a pathological cause of congenital tremors in a pig which involves determining whether the pig CC has been infected by PCV strain type II. The determination of the infection is effected by detecting the presence of a PCV nucleic acid in a biological sample from the pig, by detecting hybridisation of an oligomical optimally, the determination of infection is effected by detecting the presence of pcV polypeptide in a biological sample from the pig, by detecting the presence of antibodies discuted against a PCV polypeptide in a biological sample of the pig. An expression vector (III) encoding a PCV polypeptide is useful as a vector vaccine against congenital tremors. (II) along with a suitable adjuvant is useful as a whole PCV vaccine, while the antigenic PCV polypeptides are used as components of subunit vaccines. Antibodies against PCV proteins are useful in passive
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N-PSDB; ABU02904, ABU02910, ABU02919, ABU02926, ABU02932, ABU02939,
ABU02945, ABU02952, ABU02958, ABU02963, ABU02970.
                                                                                                                                                                                                                                                                                                                                                                                                          New porcine circovirus (PCV) nucleic acids for use as a component vaccines for treating or preventing congenital tremors in pigs.
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                                                                                                      Porcine circovirus genome; PCV; vaccine; type I PCV strain; type II PCV strain; congenital tremor; pig; whole PCV vaccine; passive immunisation; ds.
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Pred. No. 0;
0; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                             Kanitz CL;
                                                                                                                                                                                                                                                                                                                             Kiupel M,
                                                                                PMWS-Porcine circovirus (PCV) P3 genome.
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                                                                                                                                                                                                                                                                                                                             Choi
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ABX08204 standard; DNA; 1768
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Best Local Similarity 88.6*;
Matches 1455; Conservative
                                                     (first entry)
                                                                                                                                                                                                                                                                                                                             Mittal SK, Stevenson GW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes an isolated nucleic acid (I) from a porcine circovirus (PCV) where (I) comprises a sequence coding for a circovirus polypeptide. A vaccine comprising a PCV nucleic acid that encodes an
                                                                                                                   GAGAATTTAATCTTAAAGACCCCCCACTTAAACCCTAAATGAATAAAAATAAAAACATT
                                                                                                                                                                                                                                                       CIGITATICIAGAIGAIAACITIGIACCAAAGGCCAAIGCCCIAACCIAIGACCCATAIG
                                                                   511 TAAACTACTCCTCCCCCATACAATCCCCCAACCCTTCTCCTACCACTCCCGTTACTTCA
                                                                                                                                            AGCTTTGGATGAGGCTACAAACCTCTAGAAATGTGGACCACGTAGGCCTCGGCACTGCGT
                                                                                                                                                         ACGAAGTGAT --- AAAAAAGACTCAGTAATTTATTTCATATGGAAATTCAGGGCATGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU02936, ABU02938,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New porcine circovirus (PCV) nucleic acids for use as a component vaccines for treating or preventing congenital tremors in pigs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      circovirus genome; PCV; vaccine; type I PCV strain; PCV strain; congenital tremor; pig; whole PCV vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kanitz CL
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ABU02946, ABU02953, ABU02959, ABU02969, ABU02971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kiupel M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PMWS-Porcine circovirus (PCV) genome
                                                                                                                                                                                                                                                                                                                                      GGTCCACTGCTTCAAATCGGCC 1763
                                                                                                                                                                                                                                                                                                                                                               GGGAAAGGGTGACGAACTGGCC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Choi J,
                                                                                                                                                                                                                                                                                                                                                                                                                          ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                        ABX08219 standard; DNA; 1774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Porcine circovirus genome type II PCV strain; conge passive immunisation; ds.
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cuseful for treating or preventing congenital tremors in a pig or its useful for treating or preventing congenital tremors in a pig or its to useful for treating or preventing congenital tremors in a pig or its is composed of PW-15-PCV-P2, -P4, -P4, and CT-PCV-P5, -P6.

It is composed of PWWS-PCV-P2, -P5, -P4, and CT-PCV-P5, -P6.

An isolated PCV strain (II) is useful for diagnosing a pathological cause of congenital tremors in a pig which involves determining whether the pig has been infected by Strain type I or type II. The determination of the infection is effected by detecting the presence of a PCV nucleic acid of congenital sample from the pig, by detecting hybridisation of an oligonucleotide. Optionally, the determination of infection is effected by detecting the presence of PCV polypeptide in a biological sample from the pig by detecting the presence of antibodies directed against a PCV polypeptide. Optionally, the determination of infection is effected by detecting the presence of antibodies directed against a PCV polypeptide in a biological sample of the pig. An expression vector (III) encoding a CC pulphodies as vector vaccine against congenital tremors. (III) along with a suitable adjuvant is useful as a whole PCV vaccine, while the antigenic PCV properiors are useful in passive in a plantic congenital tremors.
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202/c ABX08202 standard; DNA; 1762 BP.

ABX08202

ABX08202/ ID ABX0 XX AC ABX0

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The invention describes an isolated nucleic acid (1) from a porcine circovirus (PCV) where (I) comprises a sequence coding for a circovirus polypeptide. A vaccine comprising a PCV nucleic acid that encodes an immunogenic polypeptide of type I or type II PCV strain and a carrier, is composed of PW-15-PCV and CT-PCV-P7. PCV type II s composed of PW-15-PCV and CT-PCV-P7. PCV type II is composed of PW-15-PCV and CT-PCV-P7. PCV type II is composed of PW-15-PCV-P2. -P3, -P4, and CT-PCV-P5. -P6). An isolated PCV strain (II) is useful for diagnosing a pathological cause of congenital tremors in a pig which involves determining whether the pig chas been infected by PCV strain type I or type II. The determination of the infection is effected by detecting the presence of a PCV nucleic acid in a biological sample from the pig, by detecting hybridisation of an oligonucleotide. Optionally, the determination of infection is effected by detecting binding of an antibody that specifically binds a PCV polypeptide. Optionally, the determination of infection is effected by detecting the presence of PCV polypeptide in a biological sample of the pig. An expression vector (III) encoding a PCV polypeptide is useful as a vector vaccine against congenital tremors. (II) along with a suitable adjuvant is useful as a whole PCV vaccine, while the antiable adjuvant is useful as a components of subunit concines. Antibodies against PCV proteins are useful in passive concines. Immunisation strategies. This sequence represents a porcine circovirus
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N-PSDB; ABU02908, ABU02913, ABU02917, ABU02924, ABU02931, ABU02941,
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                                                                                       Porcine circovirus genome; PCV; vaccine; type I PCV strain; type II PCV strain; congenital tremor; pig; whole PCV vaccine; passive immunisation; ds.
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Pred. No. 0;
0; Mismatches 165; Indels
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                                                      PMWS-Porcine circovirus (PCV) Pl genome
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Best Local Similarity 88.2%;
Matches 1449; Conservative
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Pred. No. 0;
0; Mismatches
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85.2%;
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Matches 1402; Conservative
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1088 1388 1448 1508 1034 CTTCAACACCCGCCTCTCCCGCACCTTCGGATATACTGTCAAGGCTACCACAGTCAGAAC 1148 GCCCTCCTGGGCGTGGACATGATGAGATTTAATATGACGACTTTGTTCCCCCGGGAGG 1208 1209 GGGGACCAACAAAATCTCTATACCCTTTGAATACTACAGAATAAGAAAGGTTAAGGTTGA 1268 ATTCTGGCCCTGCTCCCCCATCACCCAGGGTGATAGGGGAGTGGGCTCCACTGCTGTTAT 1328 GATGAGGCTACAAACCTCTAGAAATGTGGACCACGTAGGCCTCGGCACTGCGTTCGAAAA 1568 TAATCTTAAAGACCCCCACTTAAACCCTAAATGAATAAAAATAAAAACCATTACGATGT 1688 623 443 323 214 563 503 154 442 ACCTGAGCTGGACCAAACAATTGATTGGTTCCAGCCAAATAATAAAAGAAACCAGCTGTG 383 TGCAGACACACAAAATTATGTGGTAAGGCTGACTATTTATGTACAATTCAGAGAATT CTTCAATTCCCGCCTTTCTAGAGAATTTGTACTCACCATAAAAG---GAGGACACTCGCA | GCGTTACCGCAGAAGAAGAACACCGCCCCCGCAGCCATCTTGGCCAGATCCTCCGCCGCCG 859 ACCATATTTGGTACACCCCGCCTTCAGAACCGTTACAGATGGCGCCGAAGAAGAGGGTAT TCTAGATGATAACTTTGTAACAAAGGCCACAGGCCCTAACCTATGACCCATATGTAAACTA CTCCTCCCGCCATACAATCCCCAACCCTTCTCCTACCACTCCCGTTACTTCACACCCAA crecrecedecacacatraaggeaacecrirraceracerecrecaggraerreaceceaa ACCIGITCITGACTCCACCATGATTACTTCCAACCAAATAACAAAAGGAATCAGCTTTG Gerecattriaaatacecaeaeaeargreaacaeaeaeaeaeaeaeaerreeeerreeaaaa CGCTGGTAATACTACAGCAGCGCACTTCTTTCACTTTTATAGGATGACGTATCCAAGGAG cecreeraaracracaecaecacrircrircacrirraraecareaceraecaaedae CCCCTGGCTCCACCC-----CCGCCACCGCTACCGTTGGAGAAAAATGGCAT criegargccaactrigraaccccrccaccaaccresccrareaccrararraacra PK-15-Porcine circovirus (PK-15-PCV) genome. TGCTTCAAATCGGCCTTCGGGTACC 1773 TGCTTCAAATCGGCCTTCGGGTACC ΒÞ

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1459 CAGCCCGCGGAAATTTCTCACATACGTTACAGGGAACTGCTCGGCTACAGTCACCAAAGA 1400
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                                     1519 GIGTACAGCTGTCTTCCAATCACGCTGCTGCATCTTCCCGCTCACTTTCAAAGTTCAGC
                                                                      CAGCCCGCGGAAATTTCTCACATACGTTACAGAAACTGCTCGGCTACAGTCACCAAAGA
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                                                                                                                                                                                                                              CGGAGCTCCACACTCGATAAGTATGTGCCCTTCTTTACTGCAGTATTCTTTATTCTGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes an isolated mucleic acid (I) from a porcine circovirus (PCV) where (I) comprises a sequence coding for a circovirus polypeptide. A vaccine comprising a PCV nucleic acid that encodes an immunogenic polypeptide of type I or type II PCV strain and a carrier, is useful for treating or preventing congenital tremors in a pig or its progeny (PCV type I is composed of PK-15-PCV and CT-PCV-P7; PCV type II is composed of PMS-PCV-P1, PMWS-PCV-P2, -P3, -P4, and CT-PCV-P5, -P6).

An isolated PCV strain (I) is useful for diagnosing a pathological cause of congenital tremors in a pig which involves determining whether the pig considered by PCV strain type II. The determination of the infection is effected by detecting the presence of a PCV nucleic acid in a biological sample from the pig, by detecting hybridisation of an oligonucleotide. Optionally, the determination of infection is effected by detecting binding of an antibody that specifically binds a PCV polypeptide. Optionally, the determination of infection is effected by detecting the presence of antibodies directed against a PCV polypeptide in a biological sample of the pig. An averyession vector (III) encoding a PCV polypeptide is useful as a vector vaccine against congenital tremore.
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                                                                                                                                                                                                                                                                                                                                                                                                 New porcine circovirus (PCV) nucleic acids for use as a component of vaccines for treating or preventing congenital tremors in pigs.
                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABU02909, ABU02916, ABU02923, ABU02930, ABU02949, ABU02956
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Porcine circovirus genome; PCV; vaccine; type I PCV strain; type II PCV strain; congenital tremor; pig; whole PCV vaccine; passive immunisation; ds.
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                                                                                                                                                                                                                                                                                                       Kanitz CL
                                                                                                                                                                                                                                                                                                       Kiupel M,
                                                                                                                                                                                                                                                                                                       Choi J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 1; 88pp; English
                                                                                                                                                                                         15-JUN-2001; 2001WO-US019220.
                                                                                                                                                                                                                            15-JUN-2000; 2000US-0211710P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       query Match 68.3%;
Best Local Similarity 84.9%;
Matches 1397; Conservative C
                                                                                                                                                                                                                                                                                                       Mittal SK, Stevenson GW,
                                                                                                                                                                                                                                                                  (PURD ) PURDUE RES FOUND
                                                                              Porcine circovirus
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                                                                                                                                                    20-DEC-2001
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                                                                                                                                                                                  GCTCCATTTAAATACCCACACCAATGTCGAGCACACAGGCCTCGGCTATGCGCTCCAAAA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotide capable of rolling circle replication in host, useful for discovery of gene function, comprises Rep gene, sequences that are cis on the polynucleotide and open reading frame encoding protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rolling circle replication; RCR; Rep gene; gene function; Geminivirus; Circovirus; Nanovirus; gene therapy; PCV; ds.
                                                                                                                            recagecacacacaaaarrargragraagecreacrarrrargracaarraagaarr
                                                                                                                                                       TAATCTTAAAGACCCCCCCCTTAAACCCTTAAATGAATAAAATAAAATTACGATTACGATGT
                                                                                                 GATGAGGCTACAAACCTCTAGAAATGTGGACCACGTAGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       of a plasmid pCI-PCV1-Luc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence
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or in mammalian cell and thus altering or even eliminating the function of that gene, as gene sequence delivery tools for mammalian genomic approaches, for gene therapy applications (for delivering therapeutic or complementing gene products to organisms or cells), and in whole animal genomics. The present sequence represents a plasmid pCI-PCVI-Luc, comprising the PCR Rep gene and the luciferase reporter gene
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                                                                                              Sequence 7460 BP; 1910 A; 1677 C; 1886 G; 1987 T; 0 U; 0 Other;
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Rep gene; rolling circle replication; Rolling circle replicon construct pCI-CV1-luc Virucide, vaccine, gene therapy, pCI-CV1-luc, PCV, ds, luciferase.

The invention relates to a polymucleotide capable of eliciting an immunisation reaction in a eukaryotic host to a peptide or polypeptide. The polymucleotide encodes the peptide or polypeptide, and contains elements of a viral genome (i.e. the Rep gene) that is capable of rolling clical replication. The peptide or polypeptide is capable of expression in the eukaryotic host. Also included are constructing a polymucleotide capable of eliciting an immunisation reaction in a host (comprising the polymucleotide, where the polymucleotide comprises elements of a viral genome that is capable of rolling spitide or polypeptide into the capable of rolling schere levels elements of a viral genome that is capable of rolling clicle replication and immunisation and immunisation case comprising the polymucleotide into the host. Substantially higher levels of IgG antibody induction were seen in mice injected with immunogenic protein insert linked to a rolling circle replication cassette versus immunogenic protein insert linked to a rolling circle replication cassettes linked to a porcine Circovirus cassette, as compared to non-rolling circle replicance in a everyession cassettes linked to a porcine circovirus cassette, as compared to non-rolling circle replicance or gene therapy applications or for eliciting an immunisation reaction in a eukaryotic cor beta-galactosidase with substances of corplications, or for eliciting an immunisation reaction in a eukaryotic colling circle replicance or gene therapy applications, or for eliciting an immunisation reaction in a level function of that gene. The rolling circle replicance or genes the function or trait in a host eukaryotic cell, or for demandating an element or mammalian cells, which alters or even ciminates the function or trait in a host eukaryotic cell, or polymucleotide of the inventor comparising the whole PCV (porcine or polymetide. The professer elements and ä New rolling circle DNA replicons or polynucleotides, useful in vaccine gene therapy applications, for eliciting an immunization reaction in a eukaryotic host, or for inducing or enhancing a function or trait in a Sequence 7460 BP; 1911 A; 1676 C; 1887 G; 1986 T; 0 U; 0 Other; Example 2; Fig 8; 51pp; English. host eukaryotic cell. WPI; 2003-341042/32.

15; Length 7460; Indels DB 8; 192; Score 1196.8; Pred. No. 0; 0; Mismatches 67.5%; 86.8%; Matches 1357; Conservative Similarity Query Match

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for discovery of gene function, comprises Rep gene, sequences that are
cis on the polynucleotide and open reading frame encoding protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rolling circle replication; RCR; Rep gene; gene function; Geminivirus;
Circovirus; Nanovirus; gene therapy; PCV; ss.
                    Nucleotide sequence of a construct comprising the PCV Rep gene.
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Porcine circovirus.
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Example 1; Fig 5; 61pp; English.

The specification describes a polynucleotide that is capable of rolling circle replication (RCR) in an eukaryotic host. The polynucleotide congrises a Rep gene encoding from a virus, sequences that are cis on the polynucleotide such that the Rep protein can bring about RCR of the polynucleotide, an open reading frame encoding a protein of interest capable of being expressed in the host, and optionally a multiple cloning site, where the polynucleotide lacks genes of the virus. The virus is selected from the group of genera of family Geminiviridae, Circoviridae and Nanovirus The polynucleotide sequence is useful for the discovery of the function of genes in eukaryotic hosts, and for inducing or enhancing a trait in a host eukaryotic cell, for down-regulating a gene in a plant or in mammalian cell and thus altering or even eliminating the function of that gene, as gene sequence delivery tools for mammalian genomic approaches, for gene therapy applications (for delivering therapeutic or complementing gene products to organisms or cells), and in whole animal compressing the present sequence represents a construct comprising the whole products or transcriptional control of its own promoter, and has the putative coat transcriptional control of its own promoter, and has the putative coat protein inactivated by insertion of the bacterial cloning vector

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Construct 1; PCV; ds.
                                                              780 CGAAAGACGGGTATCTTCAATTCCGCCCTTTCTACAGAATTTGTACTCACCATAAAAAGA
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(MCCO/) MCCORMICK A.
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                    BP; 1216 A; 1277 C; 1514 G; 1278 T; 0 U; 0 Other;
                                                          Length 5285;
                                                      Query Match 67.4%; Score 1195.8; DB 4; Length Best Local Similarity 87.7%; Pred. No. 0; Matches 1331; Conservative 0; Mismatches 177; Indels
                    Sequence 5285
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gene therapy applications, for eliciting an immunization reaction in a eukaryotic host, or for inducing or enhancing a function or trait in a host eukaryotic cell.

Example 1; Fig 5; Slpp; English

The invention relates to a polymucleotide capable of eliciting an immunisation reaction in a eukaryotic host to a peptide or polypeptide. The polymucleotide encodes the peptide or polypeptide, and contains of elements of a viral genome (i.e. the Rep gene) that is capable of rolling contains a large of a viral genome (i.e. the Rep gene) that is capable of rolling contains a period of eliciting an immunisation reaction in a host (comprising in manufaction reaction in a host (comprising demarketic host. Also included are constructing a polymucleotide (comprising a generic encoding a peptide or polypeptide into the inserting a sequence encoding a peptide comprises elements of a viral genome that is capable of rolling circle replication and immunising a host comprising administering a composition comprising the polymucleotide into the host. Substantially higher levels of IgG antibody induction were seen in mice injected with immunogenic protein insert linked to a rolling circle replication mammalian expression vector. Levels of IgG antibody through successive bleeds were higher for both luciferase and con-rolling circle replication mammalian expression vector. Levels of IgG antibody through successive bleeds were higher for both luciferase and compared to non-rolling circle replication in a eukaryotic confirmation in a eukaryotic confirmation in a eukaryotic confirmation in a eukaryotic confirmation in a eukaryotic host is useful in vaccine or gene therapy capplication in a eukaryotic host is useful in vaccine or gene therapy capplication in a eukaryotic post is useful in vaccine or gene therapy capplication and eukaryotic nor trait in a host enkaryotic cell, or for eliciting an immunisation reaction in a eukaryotic coll, or the discovery of the function of that gene in eukaryotic host; in the polymucleotides are also useful for polymucleotide of the invention comparising the whole PCV (porcine corrollar of the invention comparising the whole PCV (proceine circuits of the invention comparising the whole contraction

Sequence 5285 BP; 1216 A; 1276 C; 1515 G; 1278 T; 0 U; 0 Other;

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1621 1561 TAGAGAGCTTCTACAGCTGGGACAGCAGTTGAGAGAGTACCATTCCTGGGGGGCCTGATTG 1741 1560 cadraddrectriaddchcaddaaarraddddchcriddchcridchadddddd 1501 300 360 181 PATGGATACCGGTCACACAGTCTCCAGTAGATCATCCCAAGGTAACCAGCCATAAAAATCA 240 CTGGTAATCAAAATACTGCGGGCCAAAAAAGGAACAGTACCCCCTTTAGTCTCTACAGTC GGGCCCACTATGACGTGTACAGCTGTCTTCCAATCACGCTGCTGCATCTTCCCGCTCACT TAGAGAGCTTCTACAGCTGGGACAGCAGTTGAGGAGTACCATTCCTGGGGGGCCTGATTG AATGGATACCGGTCACACAGTCTCAGTAGATCATCCCAAGGTAACCAGCCATAAAAATCA TCCAAAACAACTTCTTCTTCTTCCATGATATCCATCCCACCACTTATTCTACTAGGCTTC TCCAAAACAACTTCTTCTCCCATGATATCCCATCCCACTTATTTCTACTAGGCTTC CAGTAGGTGTCCCTAGGCTCAGCAAATTACGGGCCCACTGGCTCTTCCCACAACCGGGC CTGGTAATCAAAATACTGCGGGCCAAAAAAGGAACAGTACCCCCTTTAGTCTCTACAGTC GGTACCTCCGTGGATTGTTCTCCAGCAGTCTTCCAAAATTGCAAAGTAGTAATCCTCCGA Gaps 6 Length 5285; Score 1195.8; DB 8; Length Pred. No. 0; 0; Mismatches 177; Indels 67.4%; Query Match
Best Local Similarity 87.7
Matches 1331, Conservative 1860 1800 1740 1680 1620 61 121 241 301 361

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ά		TTCAAAAGTTCAGCCAGCCGGGAAATTTCTCACATACGTTACAGGAAACTGCTCGGCT 480
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ò	481	ACAGTCACCAAAGACCCCGTCTCCAAAAGGGTACTCACAGCAGTAGACAGGTCGCTGCGC 540
Dβ	1380	ACAGTCACCAAAGACCCCGTCTCCCAAAAGGGTACTCACAGCAGTAGACAGGTCGCTGCGC 1321
8 8	541	TTCCCCTGGTTCCGCGGAGCTCCACACTCGATAAGTATGTGGCCTTCTTTACTGCAGTAT 600 THIN THIN THIN THIN THIN THIN THIN THIN
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qq	1080	AGCTCCCGTATTTTGTTTTTCCTCCTCGGAAGATTATTAAGGGTGAACACCCACC
ογ	841	TTATGGGGTTGCGGGCTTTTTTTTTTTTTTTTTTTTTTT
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δ	961	ACGIAICCAAGGAGGCGTIACCGCAGAGAAGAACGCCCCCGCAGCCAICTIGGCCAG 1020
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Ğ	1021	ARCTCGGCGCCCCTGGCTCGACCCCGCCACCGCTACGTTGGAGA 1074
q _Q	840	arccrccsasaasaccararrrsscacaccccrrcasaaaccsrracasarsscs 781
Š	1075	AGGAAAATGGCATCTTCAACACCCGCCTCTCCGCACTTCGGATATACTCTCAAGGCT 1134
qq	780	cgaalgacgegtaicticaaticcegectifctacagaatitgtactcaccataaagga 721
ò	1135	ACCACAGTCAGAAGGCCCTCCTGGGGGGGGGACATGATGATATATAT
qq	720 (3GATACTCGCAGCCATCTTGGAATGTTAACTACCTCAAATTCAACATCGGCCAGTTC 664
ò	1195 (GITCCCCGGGGGGGGGGCGACCAAAATCTCTATACCCTTTGAATACTACAGAATAAGA 1254
οp	663	crececercia de caracecera e contra e contra en contra en
ģ	1255	AAGSTTAAGSTTGAATTCTGGCCCTGCTCCCCATCACCCAGGGTGATAGGGGGGGG
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<u>ئ</u>	1315	TCCACTGCTGTTATTCTAGATGATAACTTTGTAACAAAGGCCACAGGCCTAACCTATGAC 1374
qq	543	aciditatiaicricdaidecaacititoiaacecerecaecaacitigged 48
ò	1375	CCATATGTAAACTACTCCCGCCATACAATCCCCCAACCTTCTCCTACCACTCCCGT 1434
Dp	483	ccciainitiaaciaciccicceccacacataagecagectritacciaccactecage 424
È	2	ACCAAATAACAAA 14
Ωp	423	IACTICACCCCAAACCIGAGCIGGACCAAACAAITGAIIGGIICCACCCAAAIAATAAA 364

us-10-808-964a-2.rng

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The specification describes a polymucleotide that is capable of rolling circle replication (RCR) in an eukaryotic host. The polymucleotide comprises a Rep gene encoding from a virus, sequences that are cis on the polymucleotide such that the Rep protein can bring about RCR of the polymucleotide such that the Rep protein on bring about RCR of the polymucleotide such that the host, and optionally a multiple cloning site, where the polymucleotide lacks genes of the virus. The virus is selected from the group of genera of family Geminiviridae, Circoviridae and Nanovirus. The polymucleotide sequence is useful for the discovery of the function of genes in eukaryotic cell, for down-regulating a gene in a plant of that gene, as gene sequence delivery tools for mammalian cell and thus altering or even eliminating the function of that gene, as gene sequence delivery tools for mammalian gene products to organisms or cells, and in whole animal complementing gene products to organisms or cells, and in whole animal genomics. The present sequence represents a construct on which the SV40 promoter and origin of replication was deleted. This construct contains the PCV origin of replication, in the context of a vector that contains a selectable and screenable marker gene (GPP-zeocin cells).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polynucleotide capable of rolling circle replication in host, useful discovery of gene function, comprises Rep gene, sequences that are on the polynucleotide and open reading frame encoding protein of
                                                                                                                                                                                                                                                                  gene; gene function; Geminivirus; PCV; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5650 BP; 1372 A; 1333 C; 1516 G; 1429 T; 0 U; 0 Other;
                                                                                                                                                                                                                                 Nucleotide sequence of a construct comprising the PCV Rep gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1195.8; DB 4; Length
Pred. No. 0;
0; Mismatches 177; Indels
                                                                                                                                                                                                                                                                  (LARG-) LARGE SCALE BIOLOGY CORP.
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                                                                                                                       AAH74866 standard; DNA; 5650 BP
 AGGAATCAGCTTTGGAT 1511
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Best Local Similarity 87.7
Matches 1331; Conservative
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Porcine circovirus.
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                          TAGAGAGCTTCTACAGCTGGGACAGCAGTTGAGGAGTACCATTCCTGGGGGGCCTGATTG 1554
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                                                            CTGGTAATCAAAATACTGCGGGCCAAAAAGGAACAGTACCCCCTTTAGTCTCTACAGTC
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Search completed: August 5, 2005, 02:42:15 Job time: 987 sec8

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AY099495 Porcine c AY099499 Porcine c Y09921 Porcine cir

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Maximum

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Database

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FWTRLSRTFGYTVKATTVRTPSWAVDWMRFNIDDFVPPGGGTNKISIPPEYYRIRKVK
                                                                                                                                                                                                                                                                                                                                                       Porcine circovirus 2
Viruses; sBDNA viruses; Circoviridae; Circovirus.

1 (Dases 1 to 1768)

Penaux,M., Halbur,P.G., Gill,M., Toth,T.E. and Meng,X.J.

Genetic characterization of type 2 porcine circovirus (PCV-2) from pigs with postweaning multisystemic wasting syndrome in different geographic regions of North America and development of a differential PCR-restriction fragment length polymorphism assay to detect and differentiate between infections with PCV-1 and PCV-2 20341537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Virginia Tech, 1410 Prices Fork
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 1768)
Fenaux,M., Halbur,P.G., Gill,M., Toth,T.E. and Meng,X.J.
Direct Submission
                                                                                                                                                                                                                                                                                                       AF264042 1768 bp DNA linear VRL
Porcine circovirus type 2 isolate 40895 complete genome.
AF264042
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/mol type="genomic DNA"
/isolate="40895"
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Road, Blacksburg, VA 24061, USA
Location/Qualifiers
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AUTHORS
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                             Porcine circovirus 2
Viruses; seBNA viruses; Circoviridae; Circovirus.

1 (Dases 1 to 1768)

Penaux,M., Halbur,P.G., Gill,M., Toth,T.B. and Meng,X.J.

Renaux,M., Halbur,P.G., Gill,M., Toth,T.B. and Meng,X.J.

Genetic characterization of type 2 porcine circovirus (PCV-2) from pigs with postweaning multisystemic wasting syndrome in different geographic regions of North America and development of a differential PCR-restriction fragment length polymorphism assay to detect and differentiate between infections with PCV-1 and PCV-2 20341537
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Penaux,M., Halbur,P.G., Gill,M., Toth,T.E. and Meng,X.J.
Direct Submission
Submitted (08-MAY-2000) VMRCVM, Virginia Tech, 1410 Pric
Road, Blacksburg, VA 24061, USA
Location/Qualifiers
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Pred. No. 0;
0; Mismatches 151; Indels
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complement(37...738)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (37. .738)
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/note="Cap"
   GI:9392638
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larity 90.0%;
Conservative
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/gene="rep"
822. .1766
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Matches 1538; Conser
   AF264040.1
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VERSION
KEYWORDS
SOURCE
ORGANISM
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MEDLINE
PUBMED
REFERENCE
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TITLE
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TITLE
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ENTRLSRTFGYTVKRTTVTTPSWAVDWRFKLDDFVPPGGGTKKISIPPEYYR.FRVVK
VEFWPCSPITQGDRGYGSTAVILDDNFVPKATALTYDPYVNYSSRHTIPQPFSYHSRY
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                                                                                                                                                                                                                                                                                                       RITSLVFWKNATEQSTEEGGQFVTLSPPCPEFPYEINY"
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Pred. No. 0;
0; Mismatches 156; I.
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                                                                              822. .1766
/gene="rep"
822. .1766
/gene="rep"
                                                                                                                                              note="Rep"
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Viruses, sabNA viruses, Circoviridae, Circovirus.

Viruses, sabNA viruses, Circoviridae, Circovirus.

(bases 1 to 1768)

Fenaux, M., Halbur, P.G., Gill, M., Toth, T.E. and Meng, X.J.

Genetic characterization of type 2 porcine circovirus (PCV-2) from pigs with postweaning multisystemic wasting syndrome in different differential PCR-restriction fragment length polymorphism assay to detect and differentiate between infections with PCV-1 and PCV-2 20341537
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Fenaux, M., Halbur, P.G., Gill, M., Toth, T.E. and Meng, X.J.
Direct Submission
Submitted (08-MAY-2000) VWRCVM, Virginia Tech, 1410 Prices Fork
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/protein_id="AAF87229.1"
/db_xref="GI:9392636"
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Location/Qualifiers
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/organism="Porcine circovirus
/mol type="genomic DNA"
/isolate="26607"
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/gene="cap"
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/codon_start=1
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VRL 08-JUL-2002

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RESULT 4 AF520783/c LOCUS

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/product="capsid"
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/protein id="AAM76056.1"
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Anyang 6-Dong, Anyang, Gyeonggi
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Porcine circovirus type 2 isolate JHP, complete genome
                                                                                                                                                       Cha, S.H. and Choi, E.J.
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Porcine circovirus 2
Viruses abDNA viruses; Circoviridae; Circovirus. 1
1 (Dases 1 to 1768)
Park,J.H., Roh,I.S., Song,J.Y., Cha,S.H. and Choi Direct Submission
Submitted (O'T-UNN-2002) Virology Division, Nation Research and Quarantine Service, Anyang 6-Dong, A
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                                                                                                                                                                                                                                                                                             /organism="Porcine circovirus
/mol type="genomic DNA"
/isolate="JHP"
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89.8%; Pred. No. 0;
iive 0; Mismatches
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/product="replicase"
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Kim,K.M., Song,Y.K., Park,H.S. and Kang,S.Y.
Direct Submission
Submitted (08-SEP-2002) College of Veterinary Medicine, Chungk National University, #48, Gaeshin-dong, Heungduk-ku, Cheongju 361-763, Korea
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Porcine circovirus 2

Porcine discovirus 2

1 (bases; senon viruses; Circoviridae; Circovirus.

1 (bases 1 to 1768)

Fenaux, M., Halbur, P.G., Gill, M., Toth, T.E. and Meng, X.J.

pigs with postweaning multisystemic wasting syndrome in different geographic regions of North America and development of a differential PCR-restriction fragment length polymorphism assay to differential PCR-restriction infections with PCV-1 and PCV-2

J. Ciln. Microbiol. 38 (7), 2494-2503 (2000)
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Fenaux, M., Halbur, P.G., Gill, M., Toth, T.E. and Meng, X.J.
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                                                                                                    /organism="Porcine circovirus
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/isolate="40856"
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0; Mismatches
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        Direct Submission
Submitted (08-MX-2000) VMRCVM,
Road, Blacksburg, VA 24061, USA
Location/Qualifiers
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complement (37. .738)
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S Penaux, M., Halbur, P.G., Gill, M., Toth, T.E. and Meng, X.J.

Direct Submitsation

I Submitted (108-MX-2000) VMRCVM, Virginia Tech, 1410 Prices Fork
Road, Blacksburg, VA 24061, USA

Location/Qualifiers

I. .1768

/ nol type="genomic DNA"

// isoTate="26606"

/ db xref="taxon:85708"

/ country="USA: Iowa"

complement (37. .738)

/ complement (37. .738)
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                                                                          ATGTACAATTCAGAGAATTTAATCTTAAAGACCCCCCACTTAAACCCTAAATGAATAAAA 1669
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1 (bases 1 to 1768)
Fenaux,M., Halbur,P.G., Gill,M., Toth,T.E. and Meng,X.J.
Genetic characterization of type 2 porcine circovirus (PCV-2) from polgs with postweaning multisystemic wasting syndrome in different geographic regions of North America and development of a differential PCR-restriction fragment length polymorphism assay to detect and differentiate between infections with PCV-1 and PCV-2 (2011). Microbiol. 38 (7), 2494-2503 (2000)
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2 isolate 26606
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Porcine circovirus type
AP264038
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Viruses.
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GWLPWDDLLRLCDRYPLTVETKGGTVPFLARSILITSNQTPLEWYSSTAVPAVEALYR
RITSLVFWKNATEQSTEEGGQFVTLSPPCPEFPYEINY"
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                                                                                                                                                                158; Indels
                                                                                                               Score 1367.2;
Pred. No. 0;
                                                                                                                                                                0; Mismatches
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2 (bases 1 to 1768)
Fenaux,M., Halbur,P.G., Gill,M., Toth,T.E. and Meng,X.J.
Direct Submission
Submitted (08-MAY-2000) VMRCVM, Virginia Tech, 1410 Pric
Road, Blacksburg, VA 24061, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 14; Length 1768;
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Pred. No. 0;
); Mismatches 160;
                                                                                                                  /organism="Porcine circovirus
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complement(37. .738)
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89.5%; Pred
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822. .1766
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Best Local Similarity 89.5
Matches 1529; Conservative
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1 (bases 1 to 1768)
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RITSLVPWKNATEQSTEGGQFVTLSPPCPEPFININ"
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/product="putative capsid
/protein_id="AAF35301.1"
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  Length 1768;
  Score 1346.4; DB 14; Lengt
Pred. No. 0;
0; Mismatches 171; Indels
  75.9%;
Query Match 75.9
Best Local Similarity 88.9
Matches 1518; Conservative
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                                                              circular VRL 23-FBB-2000 complete genome.
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Submitted (03-NOV-1999) P24, Robert Koch Institut, Nordufer 20, Berlin 13353, Germany
Forcine circovirus 2
Porcine circovirus 2
Viruses; seDNA viruses; Circovirus.
Viruses; seDNA viruses; Circoviridae; Circovirus.
Viruses 1 to 1789
Mankertz,A., Domingo,M., Folch,J.M., LeCann,P., Jestin,A., Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D. Virus Res. 66 (1), 65-77 (2000)
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GER1,
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2 isolate (
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                                                                                                                                                                                 ATAAAAACCATTACGAAGTGATAAAAA
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Porcine circovirus type
AF201305
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822. .1766
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VERSION
KEYWORDS
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REFERENCE
AUTHORS
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88.9%; Pred. No. 0;
ive 0; Mismatches 171; Indels
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complement (37. .738)
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Porcine circovirus 2
Porcine circovirus 2
Porcine circovirus 2
Viruses; sBDNA viruses; Circoviridae; Circovirus.

1 (bases 1 to 1768)
Mankertz,A., Domingo,M., Folch,J.M., LeCann,P., Jestin,A.,
Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.
Characterisation of FCV-2 isolates from Spain, Germany and France
Virus Res. 66 (1), 65-77 (2000)
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Mankertz,A., Domingo,M., Folch,J.M., LeCann,P., Jestin,A., Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.
Subrect Submission
Submitted (03-NOV-1999) P24, Robert Koch Institut, Nordufer
Berlin 13353, Germany
1. 1768
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922. .1766
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RITSLVFWKNATEQSTEEGGGVVTLSPPCFPFYEINY"
                             1610 ATCTACAATTCAGAGAATTTAATCTTAAAGACCCCCCACTTAAACCCTAAATGAATAAAA 1669
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146 TCGGCACTGCCTTCGAAAACAGTAAATACGACCAGGACTACAATATCCGTGTAACCATGT 87
                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 1768)
Mankertz,A., Domingo,M., Folch,J.M., LeCann,P., Jestin,A.,
Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.
Direct Submission
Submitted (03-NOV-1999) P24, Robert Koch Institut, Nordufer 20,
Berlin 13353, Germany
                                                          86 Argracaarrcagagaarrraarcrraagacccccccrraaacccraaar---raara
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                                                                                                                                                                                               1768 bp DNA circular VRL 2 isolate GER2, complete genome.
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Viruses, ssDNA viruses, Circoviridae, Circovirus.
1 (bases 1 to 1768)
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complement(37..738)
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Porcine circovirus type
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/note="Rep"
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TTTATTCTGCTGATCAGTTCCCTTTCGCTTTCTCGATGTGGCAGCGGGCACCCAAATACCA 1044
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2 isolate GER3, complete genome.
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Mankertz, A., Domingo, M., Folch, J.M., LeCann, P., Jestin, A., Segalss, J., Chmielewicz, B., Plana-Duran, J. and Solke, D.
Submitssion
Submitted (03-NOV-1999) P24, Robert Koch Institut, Nordufer
                                                                                                                                                                                                                                                 And Number 1 (2010).
Mankertz.A., Domingo, M., Folch, J.M., LeCann, P., Jestin, A., Segales, J., Chmielewicz, B., Plana-Duran, J. and Soike, D. Characterisation of PCV-2 isolates from Spain, Germany and Virus Res. 66 (1), 65-77 (2000)
                                                                                                                                                                                                     Porcine circovirus 2
Porcine circovirus 2
Viruses; ssDNA viruses; Circoviridae; Circovirus.
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DB 14; Length 1768;

Score 1340; Pred. No. 0;

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Query Match Best Local Similarity

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                                      TACCTCCGTGGATTGTTCTCCAGCAGTCTTCCAAAATTGCAAAGTAGTAATCCTCCGATA
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GGAGAAGGAAAATGGCATCTTCAACACCCGCCTCCCCGCACCTTCGGATATACTGTCA 1129 	aggetaccacagtcagaacgecetectgggggggggggacatgatgagatttaatattgacg 1189 	actitigiticoccoggaggaggaccaacaaaatototatacoctitigaatactacaaa 1249 	TAAGAAAGGTTAAGGTTGAATTCTGGCCCTGCTCCCCCATCACCCAGGTGATAGGGGGG 1309 	TGGGCTCCACTGCTGTTATTCTAGATGATAACTTTGTAACAAAGGCCACAGCCCTAACCT 1369 	ATGACCCATATGTAAACTACTCCCCGCCATACAATCCCCCAACCCTTCTCCTACCACT 1429 	CCGGTTACTTCACACCAAACCTGTTCTTGACTCCACCATTGATTACTTCCAACCAA	ACAAAAGGAATCAGCTTTGGATGAGGCTACAAACCTCTAGAAATGTGGACCACGTAGGCC 1549 	TCGGCACTGCGTTCGAAAACAGTATATGACCAGGACTACAATATCCGTGTAACATGT 1609 	atgtacaattcagagaitttaatcttaaagaccccacttaaaccctaaatgaataaa 1669 	TGATAACAA 1697
1070 GGAGAAGGAAAATGGCATCT 	1130 AGGCTACCACAGTCAGAACGC 	1190 ACTTTGTTCCCCCGGGAGGGG 	1250 TAAGAAAGGTTAAGGTTGAAT: 	1310 TGGGCTCCACTGCTGTTATTCT	1370 ATGACCCATATGTAAACTACTC 	1430 CCCGTTACTTCACACCCAAACC	1490 ACAAAAGGAATCAGCTTTGGA: 	1550 TCGGCACTGCGTTCGAAAACA(1610 ATGTACAATTCAGAGAATTTA 	1670 ATAAAAACCATTACGATGTGATAACAAA
\$ 8 1	99 1	. 49 11	\$ 43 1	95 dg	8	8 8	95 43 1	95 A2	\$ 8 1	c cy

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